

```

AMSH1 THNEFTTTHVIVP--KQSAGPDYCDMENVEELFNVDQHD--LITLGWITPTQTAFLS
AMSH2 THNEFTTTHVIVP--KQSAGPDYCDMENVEELFNVDQHD--LITLGWITPTQTAFLS
AMSH MRNEFTTTHVLIP--KQSAGSDYCNTEEEELFLIQDQGG--LITLGWITPTQTAFLS
Rpn11 TVRVIDVTAMPQS--GTGVSVEAVD PVTQAKMIDMLKQIGRPEMVVGWYESSPGFGCNLS
Jab1 TMIIMDSFALPVEGTETRVNAQAAA YETAAAYENAKQVGRLENAIGWYESSPGYGCNLS
      :      :      :      :      :      :      :      :      :      :
AMSH1 SVLHTECSYQIMLPEAIAIVCSPEKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH2 SVLHTECSYQIMLPEAIAIVCSPEKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH SVLHTECSYQIMLPEESVAIVCSPEKFOETG-----FKRLTDHGLEIISCRQKGFH--PH
Rpn11 GVDINTQQSFALSERAVAVVVDPIQSVKGVVIDAFRLINAMMAVLGHEFRQTTSNLGH
Jab1 GIEVSTQMLNQFQEPTVAVVIDPTRTISAG-----KVNIGAFRTYPRGYKPEDEGPSEYQ
      : : : : : : : : : : : : : : : : : : : : : :
AMSH1 TKEPRLFSICKHV--LVKDIKI-----IVLDLR-----
AMSH2 TKEPRLFSIQKFLSGIISGTAL-----EMEPLKIGYGPNGFPLGISRSSSPSEQ
AMSH SKDPFLFCSCSHVT--VVDRAV-----TITDLR-----
Rpn11 LNKPSIQALIHGLNRHYYSITINYRKNELEQKMLLNIRKKSWMEGLITLQDYSEBCKHNS
Jab1 TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRLKLELLWKKYVWNTLSSSLTNADYTTG
      :      :      :      :      :
AMSH1 -----
AMSH2 L-----
AMSH -----
Rpn11 VVKEMLELAKNYNKA VEKEDKMTTEQLAKNVGRQDKRHLEKHVDVIMTSNIVQCLAM
Jab1 QVVDLSEKLEQSEAQIGRGSFMLG--LETHDRKSEDKLAKATRDSCKTTIEAINGLMSQV
      :
AMSH1 -----
AMSH2 -----
AMSH -----
Rpn11 LDTVVFK-----
Jab1 IKDKLFNQINIS

```

FIGURE 1

```

AMSH1 -----MEDHTDVSLSPEERVRLSKLGCNITISEDITPRR 35
AMSH2 MDQ PFTVNSLKLAAMEDHTDVSLSPEERVRLSKLGCNITISEDITPRR 50
AMSH -----MSDHGDVSLPPEDRVRLSQLGSAVEVNEIDIFPRR 35
          *.*.***.***;*****;***. ;.***.***

AMSH1 YFRSGVEMERMA SVYLEEGNLENAFVLYNKFTITLFVEKLFNHRDYQCCAV 85
AMSH2 YFRSGVEMERMA SVYLEEGNLENAFVLYNKFTITLFVEKLFNHRDYQCCAV 100
AMSH YFRSGVEIIRMA SVYSEEGNIEHAFTLYNKYITLFTEKLFKHRDYKSAVI 85
      *****; ****;* ****;*;*****;*****;*****;*****;...

AMSH1 PEKQDIMKKLKEIAFFPTDELKNDLLKKNVEYQEYLD SKNKYKAEILKK 135
AMSH2 PEKQDIMKKLKEIAFFPTDELKNDLLKKNVEYQEYLD SKNKYKAEILKK 150
AMSH PEKKDTPVKLKEIAFFPKAEIKAEILKRYTKYTYNEEKKKEAEILARN 135
      ****;* ;*****;*****;****;****;* . ** ** ;.*; * ?; ??

AMSH1 LEHQRLIEAERKRIAQMRQQQLE SEQFLFFEDQ LKQELARGQMRQQTS 185
AMSH2 LEHQRLIEAERKRIAQMRQQQLE SEQFLFFEDQ LKQELARGQMRQQTS 200
AMSH HAIQQELEKEKQKQVQAQQQLE QEQTHAFEMIRNQLEKERLKIYQEF 185
      ; *; ;* ;*;*;*** ;*****;*** **; ;*;* ; *; *

AMSH1 G-LSEQIDGSALSCFS--THQNNSLINVFADQPNKSDATNYASHSPFVNR 232
AMSH2 G-LSEQIDGSALSCFS--THQNNSLINVFADQPNKSDATNYASHSPFVNR 247
AMSH GKVDPGLGGLVPLVDLEKPSLDVFFPTLTVSSIQPSDCHTTPVRPAKPFVVD 235
      * ;. ;.*. ;. ;. ;. ;. *.* ; *.....* .;.* **;*

AMSH1 AITPAATLSAVONLVVEGLRCVVLPEDLCHKFLQLAESNIVRGLETGIL 282
AMSH2 AITPAATLSAVONLVVEGLRCVVLPEDLCHKFLQLAESNIVRGLETGIL 297
AMSH SLKPGALSNESEIPTIDGLRHVVVPGRLCPQLQLASANTARGVETGIL 285
      ;*.*. . ;. ;***** **;* ** ;*****;***;*****

AMSH1 CGKIMHNEFTITHVIVFKQSAGPDYCDMENVEE LFNVDQDHDLLITLGI 332
AMSH2 CGKIMHNEFTITHVIVFKQSAGPDYCDMENVEE LFNVDQDHDLLITLGI 347
AMSH CGKIMHNEFTITHVIVFKQSAGSDYCNTENEE LFLIQDQQLITLGI 335
      **** ;*****;*****;*****; ** ***** ;***;.*;*****

AMSH1 TPTQTAFLLSSVLLHHC SYQIMLFEAIIVCS EKHKDTGIFRLINAGML 382
AMSH2 TPTQTAFLLSSVLLHHC SYQIMLFEAIIVCS EKHKDTGIFRLINAGML 397
AMSH TPTQTAFLLSSVLLHHC SYQIMLFEAIIVCS EKHKDTGIFRLINAGML 385
      ******;*****;*****;*****;*****;*****;*****; *;

AMSH1 EVSACKKKGFHPHTKEPRLFISICKHV--LVKDIKIIVLDDL 421
AMSH2 EVSACKKKGFHPHTKEPRLFISIQKFLSGIISGTALENE PLKIGYGPNGFP 447
AMSH EISSCRQKGFHPHSDPPLFCSCSHVT--VVDRAVTTIDDL 424
      *;.*;*****;*;* **, . .; ;. ;. ;. ;. *;

AMSH1 -----
AMSH2 LLGISRSSSPSEQL 461
AMSH -----

```

FIGURE 2

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVC LG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu	LPIGMKVFGTVHSHPSPCRPSEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho	MPHDESIKGTTFHSHPSPPFPYSEGDLMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth	LPPFTGAVGSVHSHPGFVNLPAAADLHFFSKNGLFHIIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae	ISKGMIEIVGVYHSHPDHPRPSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli	IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....	HSHP''''S ''D

FIGURE 3

COP9_su5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm	VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At	AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce	EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs	TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sks1_Dd	TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRVA--VVVDPLQSVRG-KVVID
Pad1_Sc	TGRDQMVVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
.....	HSHP''''S 'D

FIGURE 4